1600

RAW SEQUENCE LISTING   DATE: 04/08/2003
PATENT APPLICATION: **US/09/859,701**   TIME: 12:16:44

Input Set : **A:\94661sequencelisting.ST25.txt**
Output Set: **N:\CRF4\04082003\I859701.raw**

```
 3 <110> APPLICANT: Warner, Benjamin P
 5 <120> TITLE OF INVENTION: Method for Detecting Binding Events Using Micro-X-Ray
 6       Fluorescence Spectrometry
 8 <130> FILE REFERENCE: S-94,661
10 <140> CURRENT APPLICATION NUMBER: 09/859,701
11 <141> CURRENT FILING DATE: 2001-05-16
13 <160> NUMBER OF SEQ ID NOS: 5
15 <170> SOFTWARE: PatentIn version 3.2
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 11
19 <212> TYPE: PRT
20 <213> ORGANISM: artificial sequence
22 <220> FEATURE:
23 <223> OTHER INFORMATION: Xaa can be His, Arg, Ser, Trp, or Tyr
26 <220> FEATURE:
27 <221> NAME/KEY: MISC_FEATURE
28 <222> LOCATION: (1)..(11)
29 <223> OTHER INFORMATION: X can be H, R, S, W, or Y
31 <400> SEQUENCE: 1
33 Xaa Gly Gly Xaa Gly Gly Xaa Gly Gly Xaa Phe
34 1               5                   10
37 <210> SEQ ID NO: 2
38 <211> LENGTH: 11
39 <212> TYPE: PRT
40 <213> ORGANISM: artificial sequence
42 <220> FEATURE:
43 <223> OTHER INFORMATION: binds strongly to methylphosphonic acid
46 <220> FEATURE:
47 <221> NAME/KEY: BINDING
48 <222> LOCATION: (1)..(11)
50 <400> SEQUENCE: 2
52 His Gly Gly His Gly Gly His Gly Gly Arg Phe
53 1               5                   10
56 <210> SEQ ID NO: 3
57 <211> LENGTH: 11
58 <212> TYPE: PRT
59 <213> ORGANISM: artificial sequence
61 <220> FEATURE:
62 <223> OTHER INFORMATION: binds strongly to methylphosphonic acid
65 <220> FEATURE:
66 <221> NAME/KEY: BINDING
67 <222> LOCATION: (1)..(11)
69 <400> SEQUENCE: 3
```

W--> (line 33)

Handwritten annotations:
pp 1-2
Does Not Comply
Corrected Diskette Needed

needs to be explained in <2207-<223> section.
See item 11 on Error Summary Sheet

FYI: Explain source of genetic material in <2207-<223> section

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```
 71 Tyr Gly Gly Tyr Gly Gly Trp Gly Gly Tyr Phe
 72 1               5                   10
 75 <210> SEQ ID NO: 4
 76 <211> LENGTH: 11
 77 <212> TYPE: PRT
 78 <213> ORGANISM: artificial sequence
 80 <220> FEATURE:
 81 <223> OTHER INFORMATION: binds to the thiol
 84 <220> FEATURE:
 85 <221> NAME/KEY: BINDING
 86 <222> LOCATION: (1)..(11)
 88 <400> SEQUENCE: 4
 90 Ser Gly Gly Arg Gly Gly His Gly Gly His Phe
 91 1               5                   10
 94 <210> SEQ ID NO: 5
 95 <211> LENGTH: 11
 96 <212> TYPE: PRT
 97 <213> ORGANISM: artificial sequence
 99 <220> FEATURE:
100 <223> OTHER INFORMATION: binds to the thiol
103 <220> FEATURE:
104 <221> NAME/KEY: BINDING
105 <222> LOCATION: (1)..(11)
107 <400> SEQUENCE: 5
109 Trp Phe Phe His Gly Gly His Gly Gly Trp Phe
110 1               5                   10
```

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 04/08/2003
PATENT APPLICATION: **US/09/859,701** TIME: 12:16:45

Input Set : **A:\94661sequencelisting.ST25.txt**
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<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 1,4,7,10

VERIFICATION SUMMARY   DATE: 04/08/2003
PATENT APPLICATION: **US/09/859,701**   TIME: 12:16:45

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L:33 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: _09/859,701_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length

Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ____ Skipped Sequences
(OLD RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences
(NEW RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10 ____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220>

Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001